

Amendments to the Claims:

Claims 1-9 are canceled.

Claims 25-36 are new.

This amendment adds, changes and/or deletes claims in this application. A detailed listing is presented of all claims that are or were in the application, irrespective of whether the claim(s) remain under examination. The text of all claims presently under examination is presented below, and all claims are presented with an appropriate defined status identifier.

Detailed and Complete Listing of Claims:

1-9. (Canceled)

10. (Withdrawn) Nucleotide sequences, characterized in that they are orthologous to the sequences responsible for all or some of the apomictic development in an apomictic form and the homologous sequences.

11. (Withdrawn) Nucleotide sequence according to claim 10, characterized in that it corresponds to a mutated elongate gene.

12. (Withdrawn) Nucleic acids containing one or more sequences as defined in claim 10 or 11, associated with the regulatory sequences necessary for expression in a plant material.

13. (Withdrawn) Cloning and expression vectors containing nucleic acids according to claim 12.

14. (Withdrawn) Cell hosts containing a vector according to claim 13.

15. (Withdrawn) Use of a sequence according to claim 10 or 11, if appropriate in conjunction with other alleles characteristic of apomictic forms, for introduction into the genome of a plant material, plant cells, plants at various stages of development and seeds, in order to impart to them an apomictic development.

16. (Withdrawn) Plant cell of Gramineae, in particular of maize, characterized in that it contains in its genome at least the part of a sequence according to claim 10 or 11 involved in an apomictic development.

17. (Withdrawn) Plant of the family of Gramineae, in particular maize, characterized in that it contains in its genome at least the part of a sequence according to claim 10 or 11 involved in an apomictic development.

18. (Withdrawn) Seed of Gramineae, in particular maize, characterized in that it contains in its genome at least part of a sequence according to claim 10 or 11 involved in an apomictic development.

19. (Withdrawn) Process for the production of apomictic plants, characterized in that a nucleotide sequence according to claim 11 is used.
20. (Withdrawn) Use of at least a part of a sequence according to claim 10 or 11 for identifying and isolating the orthologous sequences of loci in apomictic forms.
21. (Withdrawn) Hybridization probes and molecular primers, characterized in that they are compiled from a sequence according to claim 10 or 11.
22. (Withdrawn) Hybridization probes and molecular primers according to claim 18, characterized in that they are compiled from the *elongate* sequence.
23. (Withdrawn) Process for identifying and isolating genes responsible for apomeiosis in apomictic *Tripsacum*, characterized in that at least a part of the sequence of the *elongate* locus is used.
24. (Withdrawn) Process for the use of a mutagenesis population to confirm the relationship between a sequence isolated in *Tripsacum* according to claim 20 and expression of apomixis.
25. (New) A method for identifying a nucleotide segment conferring apomictic development in maize, comprising:
 - (a) identifying a locus common to *Tripsacum* and maize, wherein said locus confers an apomictic phenotype in *Tripsacum*;
 - (b) cloning a nucleotide segment that co-segregates with the apomictic phenotype; and
 - (c) verifying that said segment confers apomictic development by creating and analyzing a loss-of-function mutation.
26. (New) A method for identifying a nucleotide segment conferring apomictic development in a plant species, comprising:
 - (a) isolating a nucleotide segment conferring apomictic development in maize;
 - (b) selecting an orthologous segment in said plant species; and
 - (c) verifying that said orthologous segment confers apomictic development by creating and analyzing a loss-of-function mutation in said plant species.

27. (New) A method for producing an apomictic plant, comprising:
- (a) introducing a nucleotide segment conferring apomictic development into a plant cell;
 - (b) growing said cell under conditions suitable for plant growth; and
 - (c) selecting a plant displaying apomictic development.
28. (New) An expression vector comprising a maize nucleotide segment conferring apomictic development.
29. (New) A plant that expresses the *el11* allele and displays apomixis.
30. (New) A plant according to claim 29 that is a maize plant.
31. (New) A method for identifying a nucleotide segment conferring diplosporous development in maize, comprising:
- (a) identifying a locus common to *Tripsacum* and maize, wherein said locus confers a diplosporous phenotype;
 - (b) cloning a nucleotide segment that co-segregates with the diplosporous phenotype; and
 - (c) verifying that said segment confers diplosporous development by creating and analyzing a loss-of-function mutation.
32. (New) A method for identifying a nucleotide segment conferring diplosporous development in a plant species, comprising:
- (a) isolating a nucleotide segment conferring diplosporous development in maize;
 - (b) selecting an orthologous segment in said plant species; and
 - (c) verifying that said orthologous segment confers diplosporous development by creating and analyzing a loss-of-function mutation in said plant species.
33. (New) A method for producing a diplosporous plant, comprising:
- (a) introducing a nucleotide segment conferring diplosporous development into a plant cell;
 - (b) growing said cell under conditions suitable for plant growth; and

(c) selecting a plant displaying diplosporous development.

34. (New) An expression vector comprising a maize nucleotide segment conferring diplosporous development.

35. (New) A plant that expresses the *el1* allele and displays diplospory.

36. (New) A plant according to claim 35 that is a maize plant.